



IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/737,146

DATE: 08/27/2004

TIME: 16:51:22

Input Set : N:\Crf3\RULE60\10737146.raw

Output Set: N:\CRF4\08272004\J737146.raw

1 <110> APPLICANT: Sims, John  
 2 Born, Theresa  
 3 <120> TITLE OF INVENTION: ACPL DNA and Polypeptides  
 4 <130> FILE REFERENCE: 2872-US  
 5 <140> CURRENT APPLICATION NUMBER: US/10/737,146  
 6 <141> CURRENT FILING DATE: 2003-12-15  
 7 <150> PRIOR APPLICATION NUMBER: US/09/616,530  
 8 <151> PRIOR FILING DATE: 2000-07-14  
 9 <150> PRIOR APPLICATION NUMBER: PCT/US99/01420  
 10 <151> PRIOR FILING DATE: 1999-01-22  
 11 <150> PRIOR APPLICATION NUMBER: 60/078,835  
 12 <151> PRIOR FILING DATE: 1998-03-20  
 13 <150> PRIOR APPLICATION NUMBER: 60/072,301  
 14 <151> PRIOR FILING DATE: 1998-01-23  
 15 <160> NUMBER OF SEQ ID NOS: 7  
 16 <170> SOFTWARE: PatentIn version 3.1  
 18 <210> SEQ ID NO: 1  
 19 <211> LENGTH: 1845  
 20 <212> TYPE: DNA  
 21 <213> ORGANISM: Mus sp.  
 22 <220> FEATURE:  
 23 <221> NAME/KEY: CDS  
 24 <222> LOCATION: (1)..(1845)  
 25 <223> OTHER INFORMATION:

ENTERED

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 29 1 5 10 15  
 30 acc aca gga ttt aat cat tca gct tgt gcc acc aaa aaa ctt ctg tgg 96  
 31 Thr Thr Gly Phe Asn His Ser Ala Cys Ala Thr Lys Lys Leu Leu Trp  
 32 20 25 30  
 33 aca tat tct gca agg ggt gca gag aat ttt gtc cta ttt tgt gac tta 144  
 34 Thr Tyr Ser Ala Arg Gly Ala Glu Asn Phe Val Leu Phe Cys Asp Leu  
 35 35 40 45  
 36 caa gag ctt cag gag caa aaa ttc tcc cat gca agt caa ctg tca cca 192  
 37 Gln Glu Leu Gln Glu Gln Lys Phe Ser His Ala Ser Gln Leu Ser Pro  
 38 50 55 60  
 39 aca caa agt cct gct cac aaa cct tgc agt ggc agt cag aag gac cta 240  
 40 Thr Gln Ser Pro Ala His Lys Pro Cys Ser Gly Ser Gln Lys Asp Leu  
 41 65 70 75 80  
 42 tct gat gtc cag tgg tac atg caa cct cgg agt gga agt cca cta gag 288  
 43 Ser Asp Val Gln Trp Tyr Met Gln Pro Arg Ser Gly Ser Pro Leu Glu  
 44 85 90 95

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45	gag atc agt aga aac tct ccc cat atg cag agt gaa ggc atg ctg cat	336
46	Glu Ile Ser Arg Asn Ser Pro His Met Gln Ser Glu Gly Met Leu His	
47	100 105 110	
48	ata ttg gcc cca cag acg aac agc att tgg tca tat att tgt aga ccc	384
49	Ile Leu Ala Pro Gln Thr Asn Ser Ile Trp Ser Tyr Ile Cys Arg Pro	
50	115 120 125	
51	aga att agg agc ccc cag gat atg gcc tgt tgt atc aag aca gtc tta	432
52	Arg Ile Arg Ser Pro Gln Asp Met Ala Cys Cys Ile Lys Thr Val Leu	
53	130 135 140	
54	gaa gtt aag cct cag aga aac gtg tcc tgt ggg aac aca gca caa gat	480
55	Glu Val Lys Pro Gln Arg Asn Val Ser Cys Gly Asn Thr Ala Gln Asp	
56	145 150 155 160	
57	gaa caa gtc cta ctt ctt ggc agt act ggc tcc att cat tgt ccc agt	528
58	Glu Gln Val Leu Leu Leu Gly Ser Thr Gly Ser Ile His Cys Pro Ser	
59	165 170 175	
60	ctc agc tgc caa agt gat gta cag agt cca gag atg acc tgg tac aag	576
61	Leu Ser Cys Gln Ser Asp Val Gln Ser Pro Glu Met Thr Trp Tyr Lys	
62	180 185 190	
63	gat gga aga cta ctt cct gag cac aag aaa aat cca att gag atg gca	624
64	Asp Gly Arg Leu Leu Pro Glu His Lys Lys Asn Pro Ile Glu Met Ala	
65	195 200 205	
66	gat att tat gtt ttt aat caa ggc ttg tat gta tgt gat tac aca cag	672
67	Asp Ile Tyr Val Phe Asn Gln Gly Leu Tyr Val Cys Asp Tyr Thr Gln	
68	210 215 220	
69	tca gat aat gtg agt tcc tgg aca gtc cga gct gtg gtt aaa gtg aga	720
70	Ser Asp Asn Val Ser Ser Trp Thr Val Arg Ala Val Val Lys Val Arg	
71	225 230 235 240	
72	acc att ggt aag gac atc aat gtg aag ccg gaa att ctg gat ccc att	768
73	Thr Ile Gly Lys Asp Ile Asn Val Lys Pro Glu Ile Leu Asp Pro Ile	
74	245 250 255	
75	aca gat aca ctg gac gta gag ctt gga aag cct tta act ctc ccc tgc	816
76	Thr Asp Thr Leu Asp Val Glu Leu Gly Lys Pro Leu Thr Leu Pro Cys	
77	260 265 270	
78	aga gta cag ttt ggc ttc caa aga ctt tca aag cct gtg ata aag tgg	864
79	Arg Val Gln Phe Gly Phe Gln Arg Leu Ser Lys Pro Val Ile Lys Trp	
80	275 280 285	
81	tat gtc aaa gaa tct aca cag gag tgg gaa atg tca gta ttt gag gag	912
82	Tyr Val Lys Glu Ser Thr Gln Glu Trp Glu Met Ser Val Phe Glu Glu	
83	290 295 300	
84	aaa aga att caa tcc act ttc aag aat gaa gtc att gaa cgt acc atc	960
85	Lys Arg Ile Gln Ser Thr Phe Lys Asn Glu Val Ile Glu Arg Thr Ile	
86	305 310 315 320	
87	ttc ttg aga gaa gtt acc cag aga gat ctc agc aga aag ttt gtt tgc	1008
88	Phe Leu Arg Glu Val Thr Gln Arg Asp Leu Ser Arg Lys Phe Val Cys	
89	325 330 335	
90	ttt gcc cag aac tcc att ggg aac aca aca cgg acc ata cgg ctg agg	1056
91	Phe Ala Gln Asn Ser Ile Gly Asn Thr Thr Arg Thr Ile Arg Leu Arg	
92	340 345 350	
93	aag aag gaa gag gtg gtg ttt gta tac atc ctt ctc ggc acg gcc ttg	1104

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94	Lys	Lys	Glu	Glu	Val	Val	Phe	Val	Tyr	Ile	Leu	Leu	Gly	Thr	Ala	Leu	
95			355					360					365				
96	atg	ctg	gtg	ggc	gtt	ctg	gtg	gca	gct	gct	ttc	ctc	tac	tgg	tac	tgg	1152
97	Met	Leu	Val	Gly	Val	Leu	Val	Ala	Ala	Ala	Phe	Leu	Tyr	Trp	Tyr	Trp	
98		370					375				380						
99	att	gaa	gtt	gtc	ctg	ctc	tgt	cga	acc	tac	aag	aac	aaa	gat	gag	act	1200
100	Ile	Glu	Val	Val	Leu	Leu	Cys	Arg	Thr	Tyr	Lys	Asn	Lys	Asp	Glu	Thr	
101		385				390					395					400	
102	ctg	ggg	gat	aag	aag	gaa	ttc	gat	gca	ttt	gta	tcc	tac	tcg	aat	tgg	1248
103	Leu	Gly	Asp	Lys	Lys	Glu	Phe	Asp	Ala	Phe	Val	Ser	Tyr	Ser	Asn	Trp	
104				405						410					415		
105	agc	tct	cct	gag	act	gac	gcc	gtg	gga	tct	ctg	agt	gag	gaa	cac	ctg	1296
106	Ser	Ser	Pro	Glu	Thr	Asp	Ala	Val	Gly	Ser	Leu	Ser	Glu	Glu	His	Leu	
107			420						425					430			
108	gct	ctg	aat	ctt	ttc	ccg	gaa	gtg	cta	gaa	gac	acc	tat	ggg	tac	aga	1344
109	Ala	Leu	Asn	Leu	Phe	Pro	Glu	Val	Leu	Glu	Asp	Thr	Tyr	Gly	Tyr	Arg	
110		435						440					445				
111	ttg	tgt	ttg	ctt	gac	cga	gat	gtg	acc	cca	gga	gga	gtg	tat	gca	gat	1392
112	Leu	Cys	Leu	Leu	Asp	Arg	Asp	Val	Thr	Pro	Gly	Gly	Val	Tyr	Ala	Asp	
113		450				455					460						
114	gac	att	gtg	agc	atc	att	aag	aaa	agc	cga	aga	gga	ata	ttt	atc	ctg	1440
115	Asp	Ile	Val	Ser	Ile	Ile	Lys	Lys	Ser	Arg	Arg	Gly	Ile	Phe	Ile	Leu	
116		465			470				475						480		
117	agt	ccc	agc	tac	ctc	aat	gga	ccc	cgt	gtc	ttt	gag	cta	caa	gca	gca	1488
118	Ser	Pro	Ser	Tyr	Leu	Asn	Gly	Pro	Arg	Val	Phe	Glu	Leu	Gln	Ala	Ala	
119			485						490					495			
120	gtg	aat	ctt	gcc	ttg	gtt	gat	cag	aca	ctg	aag	ttg	att	tta	att	aag	1536
121	Val	Asn	Leu	Ala	Leu	Val	Asp	Gln	Thr	Leu	Lys	Leu	Ile	Leu	Ile	Lys	
122			500						505					510			
123	ttc	tgt	tcc	ttc	caa	gag	cca	gaa	tct	ctt	cct	tac	ctt	gtc	aaa	aag	1584
124	Phe	Cys	Ser	Phe	Gln	Glu	Pro	Glu	Ser	Leu	Pro	Tyr	Leu	Val	Lys	Lys	
125		515						520					525				
126	gct	ctg	cgg	gtt	ctc	ccc	aca	gtc	aca	tgg	aaa	ggc	ttg	aag	tcg	gtc	1632
127	Ala	Leu	Arg	Val	Leu	Pro	Thr	Val	Thr	Trp	Lys	Gly	Leu	Lys	Ser	Val	
128		530				535						540					
129	cac	gcc	agt	tcc	agg	ttc	tgg	acc	caa	att	cgt	tac	cac	atg	cct	gtg	1680
130	His	Ala	Ser	Ser	Arg	Phe	Trp	Thr	Gln	Ile	Arg	Tyr	His	Met	Pro	Val	
131		545				550					555					560	
132	aag	aac	tcc	aac	agg	ttt	atg	ttc	aac	ggg	ctc	aga	att	ttc	ctg	aag	1728
133	Lys	Asn	Ser	Asn	Arg	Phe	Met	Phe	Asn	Gly	Leu	Arg	Ile	Phe	Leu	Lys	
134			565						570					575			
135	ggc	ttt	tcc	cct	gaa	aag	gac	cta	gtg	aca	cag	aaa	ccc	ctg	gaa	gga	1776
136	Gly	Phe	Ser	Pro	Glu	Lys	Asp	Leu	Val	Thr	Gln	Lys	Pro	Leu	Glu	Gly	
137			580						585					590			
138	atg	ccc	aag	tct	ggg	aat	gac	cac	gga	gct	cag	aac	ctc	ctt	ctc	tac	1824
139	Met	Pro	Lys	Ser	Gly	Asn	Asp	His	Gly	Ala	Gln	Asn	Leu	Leu	Leu	Tyr	
140		595						600					605				
141	agt	gac	cag	aag	agg	tgc	tga										1845
142	Ser	Asp	Gln	Lys	Arg	Cys											

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143          610
145 <210> SEQ ID NO: 2
146 <211> LENGTH: 614
147 <212> TYPE: PRT
148 <213> ORGANISM: Mus sp.
149 <400> SEQUENCE: 2
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153 20 25 30
154 Thr Tyr Ser Ala Arg Gly Ala Glu Asn Phe Val Leu Phe Cys Asp Leu
155 35 40 45
156 Gln Glu Leu Gln Glu Gln Lys Phe Ser His Ala Ser Gln Leu Ser Pro
157 50 55 60
158 Thr Gln Ser Pro Ala His Lys Pro Cys Ser Gly Ser Gln Lys Asp Leu
159 65 70 75 80
160 Ser Asp Val Gln Trp Tyr Met Gln Pro Arg Ser Gly Ser Pro Leu Glu
161 85 90 95
162 Glu Ile Ser Arg Asn Ser Pro His Met Gln Ser Glu Gly Met Leu His
163 100 105 110
164 Ile Leu Ala Pro Gln Thr Asn Ser Ile Trp Ser Tyr Ile Cys Arg Pro
165 115 120 125
166 Arg Ile Arg Ser Pro Gln Asp Met Ala Cys Cys Ile Lys Thr Val Leu
167 130 135 140
168 Glu Val Lys Pro Gln Arg Asn Val Ser Cys Gly Asn Thr Ala Gln Asp
169 145 150 155 160
170 Glu Gln Val Leu Leu Leu Gly Ser Thr Gly Ser Ile His Cys Pro Ser
171 165 170 175
172 Leu Ser Cys Gln Ser Asp Val Gln Ser Pro Glu Met Thr Trp Tyr Lys
173 180 185 190
174 Asp Gly Arg Leu Leu Pro Glu His Lys Lys Asn Pro Ile Glu Met Ala
175 195 200 205
176 Asp Ile Tyr Val Phe Asn Gln Gly Leu Tyr Val Cys Asp Tyr Thr Gln
177 210 215 220
178 Ser Asp Asn Val Ser Ser Trp Thr Val Arg Ala Val Val Lys Val Arg
179 225 230 235 240
180 Thr Ile Gly Lys Asp Ile Asn Val Lys Pro Glu Ile Leu Asp Pro Ile
181 245 250 255
182 Thr Asp Thr Leu Asp Val Glu Leu Gly Lys Pro Leu Thr Leu Pro Cys
183 260 265 270
184 Arg Val Gln Phe Gly Phe Gln Arg Leu Ser Lys Pro Val Ile Lys Trp
185 275 280 285
186 Tyr Val Lys Glu Ser Thr Gln Glu Trp Glu Met Ser Val Phe Glu Glu
187 290 295 300
188 Lys Arg Ile Gln Ser Thr Phe Lys Asn Glu Val Ile Glu Arg Thr Ile
189 305 310 315 320
190 Phe Leu Arg Glu Val Thr Gln Arg Asp Leu Ser Arg Lys Phe Val Cys
191 325 330 335
192 Phe Ala Gln Asn Ser Ile Gly Asn Thr Thr Arg Thr Ile Arg Leu Arg

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193          340          345          350
194  Lys Lys Glu Glu Val Val Phe Val Tyr Ile Leu Leu Gly Thr Ala Leu
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196  Met Leu Val Gly Val Leu Val Ala Ala Ala Phe Leu Tyr Trp Tyr Trp
197          370          375          380
198  Ile Glu Val Val Leu Leu Cys Arg Thr Tyr Lys Asn Lys Asp Glu Thr
199          385          390          395          400
200  Leu Gly Asp Lys Lys Glu Phe Asp Ala Phe Val Ser Tyr Ser Asn Trp
201          405          410          415
202  Ser Ser Pro Glu Thr Asp Ala Val Gly Ser Leu Ser Glu Glu His Leu
203          420          425          430
204  Ala Leu Asn Leu Phe Pro Glu Val Leu Glu Asp Thr Tyr Gly Tyr Arg
205          435          440          445
206  Leu Cys Leu Leu Asp Arg Asp Val Thr Pro Gly Gly Val Tyr Ala Asp
207          450          455          460
208  Asp Ile Val Ser Ile Ile Lys Lys Ser Arg Arg Gly Ile Phe Ile Leu
209          465          470          475          480
210  Ser Pro Ser Tyr Leu Asn Gly Pro Arg Val Phe Glu Leu Gln Ala Ala
211          485          490          495
212  Val Asn Leu Ala Leu Val Asp Gln Thr Leu Lys Leu Ile Leu Ile Lys
213          500          505          510
214  Phe Cys Ser Phe Gln Glu Pro Glu Ser Leu Pro Tyr Leu Val Lys Lys
215          515          520          525
216  Ala Leu Arg Val Leu Pro Thr Val Thr Trp Lys Gly Leu Lys Ser Val
217          530          535          540
218  His Ala Ser Ser Arg Phe Trp Thr Gln Ile Arg Tyr His Met Pro Val
219          545          550          555          560
220  Lys Asn Ser Asn Arg Phe Met Phe Asn Gly Leu Arg Ile Phe Leu Lys
221          565          570          575
222  Gly Phe Ser Pro Glu Lys Asp Leu Val Thr Gln Lys Pro Leu Glu Gly
223          580          585          590
224  Met Pro Lys Ser Gly Asn Asp His Gly Ala Gln Asn Leu Leu Leu Tyr
225          595          600          605
226  Ser Asp Gln Lys Arg Cys
227          610

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229 &lt;210&gt; SEQ ID NO: 3

230 &lt;211&gt; LENGTH: 754

231 &lt;212&gt; TYPE: DNA

232 &lt;213&gt; ORGANISM: Homo sapiens

233 &lt;220&gt; FEATURE:

234 &lt;221&gt; NAME/KEY: misc\_feature

235 &lt;222&gt; LOCATION: (6)..(8)

236 &lt;223&gt; OTHER INFORMATION: "n" = a, t, c, g

237 &lt;221&gt; NAME/KEY: misc\_feature

238 &lt;222&gt; LOCATION: (563)..(563)

239 &lt;223&gt; OTHER INFORMATION: "n" = a, t, c, g

W--&gt; 240 &lt;221&gt; misc\_feature

241 &lt;222&gt; LOCATION: (596)..(596)

242 &lt;223&gt; OTHER INFORMATION: "n" = a, t, c, g

## RAW SEQUENCE LISTING ERROR SUMMARY

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Input Set : N:\Crf3\RULE60\10737146.raw

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 6,7,8,563,596,607,708,729,752

**VERIFICATION SUMMARY**

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Input Set : N:\Crf3\RULE60\10737146.raw

Output Set: N:\CRF4\08272004\J737146.raw

L:26 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:0  
L:240 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3  
L:243 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3  
L:246 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3  
L:249 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3  
L:252 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3  
L:255 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3  
L:256 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0  
M:341 Repeated in SeqNo=3  
L:303 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:0